

# FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC  
TGTGCCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT  
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCCGGC  
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTGAGCAGCCGGAAGCAGAGAATGTGGACCAG  
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA  
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC  
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG  
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC  
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC  
CATCTCCTGGCTTCAGTCCTTACAATGTGAGTAAACAGCCTTGCTGGGCCTGACCAAGACC  
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA  
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC  
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTCTCTGTGCTCT  
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT  
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCCTGC  
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT  
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTCTGCT  
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT  
GAGTCTACCTTGGCAAAGACCAAGATATTTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA  
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG  
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

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Atty Docket: GNE.2930R1C10C1

## **FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVS  
SRKQQNVVDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG  
SIMDVTEEVWDKTLTDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK  
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC  
AGIVSFLCSEDASYITGETVVVGGGTPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation site.**

amino acids 183-186

**N-myristoylation sites.**

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 276-278

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ACIDS ENCODING THE SAME*

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*Appl. No.: Not Yet Assigned*

*Atty Docket: GNE.2930R1C10C1*

# FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCGATAGCGGCATCGAGAGCGCCTCCGTCGAGGACCAGGCGGCG  
 CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGCGCAGCAGCTGCTGACCCTGCAGAACAGGTGGC  
 GCGGCTGGAGGAGGAGAACCAGAGACTTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAACTGC  
 AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAAGTGCAGGCTGCGGCTGCGGTTAGAGCTGGTGCGG  
 CCAGGCTGGGGGGGCTGCGGCTCCTGAATGGCTGCCTCCCGGGTCCCTTTGTGCTCGACCTCATAC  
 AGCCCCCTGGGGGGTGCCACGCCCATGTGCTGGGCATGGTGCCGCTGCCTGCCTCCCTGGAGATG  
 AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT  
 GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGAGCCGCC  
 CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGCGACGCCAG  
 GGAGTCTGCCAGAGAGGAAGGGCCAGAGCTTTGCCCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC  
 AGAGCAGTTGGTGGGAGCAAGGCCCCGAGTTGAGGCCCCGAGGTCCCCCTGCCACAGCCTCAGAGTG  
 GCGGCTGGCCAGGCCCAGCAGAAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA  
 TTGGCGAGCTGGTCCGCACAGGAAAGGCAGCTCAGGCCCTGAACGCCAGCACAGCCAGCGTATCCGG  
 GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT  
 CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGCAGGAGGGTCCGCTG  
 CGGCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTGCG  
 GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGCGGACA  
 GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC  
 AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAAGATCCTGAAGATTAAGACGGAA  
 GAGATCGCGGCCCTTCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTTCAGCCTGGAACAGCA  
 GCAGAAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG  
 CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG  
 CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG  
 AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA  
 GCGCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC  
 AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCGAGGAGGAGCGGAC  
 GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA  
 CATGCCGCCAGCGGGTGCTTCGGGCCCTCAGCCTCGTTGCTGTCCAGTGCGAGATGAACCTCATGGCC  
 AAGCTCAGCTACCTCTCATCCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC  
 GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCTTCTCGGAACTGGAGATGCAGCTGGAGGAGCAGC  
 AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC  
 CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA  
 AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAAGTGGGCCGTT  
 ACATGTGGATAAACAGGAACTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT  
 GGGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTGGC  
 ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGACT  
 TGGTCCACGCTCCGTTACCTTGACCTGGAACGCTCGAGCCTGTGTGGTGGAGGAGCAGGGGTCCCCC  
 GAGGAACTGAGGCAGCGGGAGGCGGCTGAGCCCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG  
 CCTGCCCTGGAACCTTGGGCCTTTGTCCAAGCCCCGGCGGGAAGTGCAGCAGGAGCCAGCCGGGGATGA  
 TTGATGTCCGGAACCCCTGTAAGCCCTCGGGGCGAGACCCTGCCTTGGAGGGAGACTCCGAGCCT  
 GCTGAAAGGGGCGAGCTGCCTGTTTGTCTTCTGTGAAGGGCAGTCCTTACCGCACACCCTAAATCCAGG  
 CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCAAAAGAACTGGACCCTCATTT  
 AACAAAATAATATGCAAAATCCCACCACTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCTTGTG  
 TCTTGCTCGAATCTCAGGACAATTCTGGTTTCAGGCGTAAATGGATGTGCTTGTAGTTTCAAGGGTTTG  
 GCCAAGAATCATCACGAAAGGGTCGGTGGCAACCAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG  
 GAAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAATCTTTGAAGGGAC

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

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Appl. No.: Not Yet Assigned

Atty Docket: GNE.2930R1C10C1

## FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLLELVRPGWGGLRLLNGLPPGSFVPRPHTAPLGGAHAHV  
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL  
HLRRNRISNCSQRAGARPGSLPERKGPELCLEELDAAIPGSRAVGGSKARVQARQVPPATAS  
EWRLAQAAQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE  
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE  
LERNVQLMRQQQGQLQRRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA  
AFQRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQQRRALEELGEELHKREAILAKKE  
ALMQEKTGLESKRRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSQAQSQQQIRGEIDS  
LRQEKDSSLKQRLLEIDGKLRLQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQVLR  
ASASLLSQCEMNLMAKLSYLSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR  
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQRDHLGEGGLADSRRQYEARIQALEK  
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG  
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG  
PLSKPRRELRRASPGMIDVRKNPL

### **Important features:**

**Leucine zipper pattern.**

amino acids 557-579, 794-815

**N-glycosylation sites.**

amino acids 133-136, 383-386

**Kinesin related protein Kif-4 Coiled-coil domain:**

amino acids 231-672

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Atty Docket: GNE.2930R1C10C1

## **FIGURE 5**

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT  
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA  
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG  
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT  
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG  
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCATTATCTCCCATCTCCCGGAGCTGTAC  
CAGGAACAGGAGGCACGTCTGTACCCATAAAAACCCAGGCTCCACTGGCAGACGGCAGAC  
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA  
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC  
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG  
AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

*SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME*

*Botstein, et al.*

*Appl. No.: Not Yet Assigned*

*Atty Docket: GNE.2930R1C10C1*

## FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQCSKGTTDAPVGSGWLWCQPTPRCGNKIYNPSEQCCYDDAILS  
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSTRNRRHVLYP

**Important features:**

**Signal sequence**

amino acids 1-21

**N-myristoylation sites.**

amino acids 33-39, 70-76

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ACIDS ENCODING THE SAME

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Atty Docket: GNE.2930R1C10C1

## FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT  
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG  
AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG  
GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT  
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCG  
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG  
TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCGCTGCTACCCCTG  
CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG  
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCGCCC  
GCCCCGCCGGGACGTGGTAGGGGATGCCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA  
GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG  
AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG  
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT  
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC  
TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC  
CCCGCAGGCGGAAGCCCTGGCCGCAGCCGCCCAGGACGCGATTGGCCCCGGAACCTGCGCCCCA  
CGCCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGAAGGGCTGCGTGAGCAG  
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCT  
GTGCACCGAGGAGGGGCGGCTGTGCGCGCAGCCGAGTGCCCGAGGCTGCACCCGCGCTGCA  
TCCACGTGACACGAGCCAGTGCTGCCCCGAGTGCAAGGAGAGGAAGAATACTGCGAGTTC  
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTG  
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACC  
CTGTGTACGAGCCTGATCAGTGCTGTCCCACTCTGCAAAAATGGTCCAAACTGCTTTGCAGAA  
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC  
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC  
AAATGTAGACGCTTCCCAGAACACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA  
CATTCTAGATGACTCTGGGAACTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA  
TTGTTGGTACTTTTCCTTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTT  
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG  
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG  
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

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Appl. No.: Not Yet Assigned

Atty Docket: GNE.2930R1C10C1

## FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL  
GRPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPOAEALA  
AAAQDAIGPELAPTPEPPPEEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPCLCTEEGPL  
CAQPECPR LHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCCEANGEVL  
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEETWR  
IERQAMCTRHECRQM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187

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ACIDS ENCODING THE SAME

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Atty Docket: GNE.2930R1C10C1



## FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC  
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG  
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA  
ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAAC  
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG  
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCGTGCCAGGAGACCGGCAGTGTC  
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
GGCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAAT  
GAGCATTGAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG  
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
GTGGGGAGTGGTTTGCCCTTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA  
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCC'ITGGACACCAGATTCTTTC  
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATCTACTCACCTAACAGCA  
AACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

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ACIDS ENCODING THE SAME

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## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRGGRGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL  
LLIDVGLTSTLVGTCGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSTQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 243-260

**N-glycosylation sites.**

amino acids 46-49, 189-192, 382-385

**Glycosaminoglycan attachment sites.**

amino acids 51-54, 359-362

**N-myristoylation sites.**

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,  
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,  
360-365, 361-366, 388-393, 408-413, 419-424

*SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME*

*Botstein, et al.*

*Appl. No.: Not Yet Assigned*

*Atty Docket: GNE.2930R1C10C1*

## FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG  
GCTGCGGGCGTCTCTCGTCGCTTGCGCGCTGCTCTTCTAGAGCCGAGGGACCCGGTGGC  
CTCGTCGCTCAGCCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT  
TGTCGGGCCCCGAGGCTCCGTGGCGGGACCCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG  
CAGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT  
GAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCG  
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC  
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT  
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGC  
ACCGCTGCATGGATAGCAGCGCCGCTTCTTGCAGGGGCTGTGGCAGCACTACCACCCTGGC  
TTGCCGCCCGCGGACGTCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT  
GAGATTTTTTGTACTGTGAGAAGTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTT  
ATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCT  
ACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTACCTG  
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATG  
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTAT  
ACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGC  
AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG  
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA  
GCGTACAATTACAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGC  
CTCGAACCTGATATTTGTGCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACATTTCC  
GAGTGCAGATGTTATTAAATGAAAAGGTGTACCTTTGGCTTACTCACAAGAACTGTTTCA  
TTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTTCAGAGTTGTCAAACAGTGAAGA  
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACATATGAGTAACTGAAGAACATTTTT  
AATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAAATAGGTAGGCAATTCCTTGATT  
ACAGGAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTACAGAAAAACATTGGGTTTCTC  
TCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAA  
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCCTCCTAC  
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTATAATAACACTTGAAAAGTGCT  
GGAGTAACAAAATATCTCAGTTGGACCATCCTTAACCTTGATTGAACTGTCTAGGAACTTTAC  
AGATTGTTCTGCAGTTCTCTCTTTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC  
AGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT  
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA  
TGAAAATAAATATTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT  
TTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC  
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTTATTCTGT  
CACTTGGCTTCGATTTTTATATTTTCTTATTATATGAAATGTATCTTTTGGTTGTTTGATTT  
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA  
TAAAGAAAATTCTTGTGACTTTAAAAA

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

Botstein, et al.

Appl. No.: Not Yet Assigned

Atty Docket: GNE.2930R1C10C1

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLS  
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS  
RDLGAALADWPLWYADWMDGQLVKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR  
CMDSSAAFLQGLWQHYPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH  
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSDLAIKGVKSPWCDVFDIDDA  
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE  
TLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV  
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDDEL

### **Important features:**

#### **Signal sequence**

amino acids 1-30

#### **N-glycosylation sites.**

amino acids 242-246, 481-485

#### **N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

#### **Endoplasmic reticulum targeting sequence.**

amino acids 484-489

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ACIDS ENCODING THE SAME

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# FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACCTGTCTTGATCATTACGGATTTCGC  
AGACAAGTGACCCAGGATCGAGTGGAGAAATTCAGATGAACAAACCACATATGTGTTTTTTGACAACAAA  
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTGCTTGTCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCAGTAGGCAACACTGC  
CCAGAGCCAATCCAGATTTTCGCAATTCTTCTTCCACTTAAACTCTGAAACAGGCACCTTGGTGTTCCTGCTG  
TTCACAAGGACGACTCTGGGCGAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTTGGGGGGGTTCTGGTTGTCTTGTCTGACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTCTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTTCTGGCCTGATTCGCCGATGAGTATTAGG  
GTGATCTTAAAGAGTTTGTCTACGTAAACGCCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCACTACTGGTCTGT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTGTCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAACAAACCAAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGATTAAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTATTATTTATAAAATTT  
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTTTTAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAAGAGTATTTTACCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCCCTTTCT  
CACACAAGTTTTAGCCTTTTTCAGAAGGGAATCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCCAGTTAAGCAATGTTGAAATCAGTTGTCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCCGCTCTAGCTCACTGTTGCCCTCGCTGTCTGCGAGGAGGCCCT  
GCCATCCTTGGGCCCCGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTAAATATTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCCTGTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAAGCAGTTTCTAATTTTGACTTTAAATTTTTTATCCGCCGAGACACTGCTCCCAT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTCTGTAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTTCACTTCCAGTGTCTTGGGTTTTTTTATACCTTTGACAGCTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTCTAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA  
TGGGAACCCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTGTTTAAAC  
CTCATTTATAAAAGCTTCAAAAAAACCCA

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

Botstein, et al.

Appl. No.: Not Yet Assigned

Atty Docket: GNE.2930R1C10C1

## **FIGURE 14**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG  
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

Botstein, et al.

Appl. No.: Not Yet Assigned

Atty Docket: GNE.2930R1C10C1

Atty Docket: GNE.2930R1C10C1

## FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPPEEKPLPTAFLVDTSEEALLLPDWLKLRM  
IRSEVLRRLVDAALQDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY  
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG  
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL  
ATLLSSPHGGALVMSMHRSHFLACPLLRLQCQYQRCVPQDTGFSSFLKVLQMLQWLDSFG  
VEGGPLRAQLRMLASQASAGRRRLSDVRGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ  
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASFPACKPVVVSSLLLQEEEP  
GGKPGADGGSLEAVRLGPSSGLLVLDWLEMLDPEVVSSCPDLQLRLLFSRRKGGKGAQVPSFR  
PYLLTLFTHQSSWPTLHQCIQVLLGKSREQRFDPSASLDFLWACIHVPRIWQGRDQRTQKR  
REELVLRVQGPELISLVELILAEAETRSQDGDTAACSLIQARLPLLLSCCGDDESVRKVTE  
HLSGCIQQWGDVSLGRRCDLLQLYLQRPVPEVLLHSEGAASSSVCKLDGLIHRFI  
TLLADTSDSRALENRGADASMACKLAVAHPLLLRHLPMIAALLHGRTHLNFQEFQQNHL  
SCFLHVLGLLELLQPHVFRSEHQGALWDCLLSFIRLLNRYKSSRHLAAFINKFVQFIHKYI  
TYNAPAAISFLQKHADPLHDLSFDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG  
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSDIDEMSRRRPEILSFFSTNLQRL  
MSSAECCRNLAFLSLALRSMQNSPSIAAFLPTFMVCLGSQDFEVVQTALRNLPYALLCQE  
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

**Important features:**

**Signal peptide:**

amino acids 1-16

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

**N-myristoylation sites.**

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,  
665-671, 698-704

**Amidation sites.**

amino acids 329-333, 634-638

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

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Appl. No.: Not Yet Assigned

Atty Docket: GNE.2930R1C10C1



## FIGURE 17

CCGGGCCATGCAGCCTCGGCCCCGCGGGCGCCCGCCGCGCACCCGAGGAGATGAGGCTCCGC  
AATGGCACCTTCCTGACGCTGCTGCTCTTCTGCCTGTGCGCCTTCCTCTCGCTGTCTGGTA  
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTCTTGGCGC  
TGC GCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG  
GTGCTGGACGAGATCAAGAGGGCCGTGTGAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA  
TCGCACCTGGGGCCGCTAACAGAGGACCCCGATTGAAGCCGTGGAACGGCTCACACCGGC  
ACGTGCTGCACCTGCCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT  
CTGCAGCCCGCGGTGCGCGTGGGCCAGGGCCGACCCGAGTGTGCGTGGTGATGGGCATCCC  
GAGCGTGGGCGCGAGGTGCACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC  
TGAGCCCGCAGGAGAAGGAGGACTCGGTGATCGTGGTGCTGATCGCCGAGACTGACTCACAG  
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGGAGATCCATTCTGGGCT  
CCTGGAGGTGATCTCACCTCCCCCACTTCTACCCTGACTTCTCCCGCCTCCGAGAGTCCT  
TTGGGGACCCCAAGGAGAGAGTCAGGTGGAGGACCAACAGAACCTCGATTACTGCTTCCTC  
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA  
GCCCCAATACCTGAGCACCATGAAGAACTTTGCACTGCAGCAGCCTTCAGAGGACTGGATGA  
TCCTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG  
ATTGTAGAGTTCATTCTCATGTTCTACCGGGACAAGCCCATCGACTGGCTCCTGGACCATAT  
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA  
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACTCACTCCTCGCTGGCT  
GGCAAGATCCAGAACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT  
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATACCAGCACTTCACCCTGGAGAAAG  
CCTACCTGCGCGAGGACTTCTTCTGGGCCTTCACCCCTGCCGCGGGGGACTTCATCCGCTTC  
CGCTTCTTCCAACCTCTAAGACTGGAGCGGTTCTTCTTCCGCAGTGGGAACATCGAGCACCC  
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCCCTCAGTCAGACA  
AGGAGGCCCTGCAGGAGGGCCGACCCGCCACCCTCCGGTACCCTCGGAGCCCCGACGGCTAC  
CTCCAGATCGGCTCCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCC  
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGAATCCCCTGTGTGGGTGATTCTGAGCGAGA  
TCTTCTGAAAAAGGCCGACTAAGCTGCGGGCTTCTGAGGGTACCCTGTGGCCAGCCCTGAA  
GCCCACATTTCTGGGGGTGTGCTCACTGCCGTCCCCGGAGGGCCAGATACGGCCCCGCCAA  
AGGGTTCTGCCTGGCGTCGGGCTTGGGCCGGCCTGGGGTCCGCCGCTGGCCCGGAGGCCCTA  
GGAGCTGGTGCTGCCCCCGCCCGCCGGGCGCGGAGGAGGCAGGCGGCCCCCACACTGTGCC  
TGAGGCCCCGAACCGTTCGCACCCGGCCTGCCCCAGTCAGGCCGTTTTAGAAGAGCTTTTAC  
TTGGGCGCCCGCGTCTTGGCGCGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT  
TTTTATTCTTGGATACATTTGATTTTTTTCACGTAAGTCCACATATACTTCTATAAGAGCGTG  
ACTTGTAATAAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

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Appl. No.: Not Yet Assigned

Atty Docket: GNE.2930R1C10C1

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRHLHAAEQESLKRSK  
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA  
KESSLQPAVRVGQGRITGVSVVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE  
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVWRWTKQNLD  
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL  
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT  
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD  
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPPDNPQSDKEALQEGRTATLRYPRS  
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

### **Important features:**

#### **Signal sequence**

amino acids 1-23

#### **N-glycosylation sites.**

amino acids 5-9, 87-91, 103-107, 465-469

#### **N-myristoylation sites.**

amino acids 6-12, 136-142, 370-376, 509-515

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

Botstein, et al.

Appl. No.: Not Yet Assigned

Atty Docket: GNE.29301C10C1